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(54) Title: VACCINE COMPOSITIONS COMPRISING THE <i>HELICOBACTER PYLORI</i> FlgE POLYPEPTIDE (57) Abstract The present invention relates to polypeptides and vaccine compositions for inducing a protective immune response to <i>Helicobacter pylori</i> infection. The invention furthermore relates to the use of <i>Helicobacter pylori</i> polypeptides in the manufacture of compositions for the treatment or prophylaxis of <i>Helicobacter pylori</i> infection.		

VACCINE COMPOSITIONS COMPRISING THE *HELICOBACTER PYLORI* FigE POLYPEPTIDE

TECHNICAL FIELD

5 The present invention relates to polypeptides and vaccine compositions for inducing a protective immune response to *Helicobacter pylori* infection. The invention furthermore relates to the use of *Helicobacter pylori* polypeptides in the manufacture of compositions for the treatment or prophylaxis of *Helicobacter pylori* infection.

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BACKGROUND ART

Helicobacter pylori

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The gram-negative bacterium *Helicobacter pylori* (*H. pylori*) is an important human pathogen, involved in several gastroduodenal diseases. Colonization of gastric epithelium by the bacterium leads to active inflammation and progressive chronic gastritis, with a greatly enhanced risk of progression to peptic ulcer disease. A
20 lifelong inflammation of the gastric mucosa is very closely correlated with a significantly enhanced risk for gastric cancer.

In order to colonize the gastric mucosa, *H. pylori* uses a number of virulence factors. Such virulence factors comprise several adhesins, with which the
25 bacterium associates with the mucus and/or binds to epithelial cells; urease which helps to neutralize the acid environment; and proteolytic enzymes which makes the mucus more fluid. In addition *H. pylori* is highly motile, swimming in the mucus and down into the crypts. Motility has been shown to be an essential virulence factor, since non motile *H. pylori* has failed to infect the mucosa in
30 experimental models Eaton et al. (Infection & Immunity 64(7), 2445-2448, 1996).

There are many possible reasons for this, the most obvious being an inability to swim down and attach to mucosal cells and the inability to avoid noxious agents in the stomach.

- 5 Despite a strong apparent host immune response to *H. pylori*, with production of both local (mucosal) as well as systemic antibodies, the pathogen persists in the gastric mucosa, normally for the life of the host. The reason for this is probably that the spontaneously induced immune-responses are inadequate or directed towards the wrong epitopes of the antigens. Alternatively the immune response
10 could be of the wrong kind, since the immune system might treat *H. pylori* as a commensal (as indicated from the life-time host/bacteria relationship).

- In order to understand the pathogenesis and immunology of *H. pylori* infections, it is of great importance to define the antigenic structure of this bacterium. In
15 particular, there is a need for characterization of surface-exposed, surface associated as well as secreted proteins which, in many bacterial pathogens, have been shown to constitute the main virulence factors, and which can be useful for the diagnosis of *H. pylori* and in the manufacture of vaccine compositions. If such proteins in addition to being surface associated also are essential for survival
20 and/or colonization their usefulness as a target for vaccine mediated immunotherapy targets increase.

- Whenever stressed or threatened, the *H. pylori* cell transforms from a bacillary to a coccoid form. In the coccoid form, the *H. pylori* cell is much less sensitive to
25 antibiotics and other anti-bacterial agents. Circumstantial evidence indicate the *H. pylori* might be transmitted between individuals in this form, possibly via water or direct contact (oral-oral; faecal-oral). An efficient vaccine composition should therefore elicit an immune response towards both the coccoid and the bacillary form of *H. pylori*. Since systemic immunity probably only plays a limited role in

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protection against mucosal infections, it is also important that the vaccine composition will enhance protective immune mechanisms locally in the stomach.

Flagellar Hook protein

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Flagellar hooks from *H. pylori* has been shown to be composed of FlgE subunits of 78 kDa (O'Toole et al. Molecular Microbiology, 14(4), 691-703, 1994). The role of the flagellar hook is to connect the flagella with the submembraneous flagellar motor. The part of the hook extruding outside the membrane is short,
10 approximately 60 nanometers (compared to approximately 10 micrometers for the flagella). Like the fagellum of *H. pylori* the hook is probably covered with a sheet (Geis et al. (1993) J. Med. Microbiol. 38(5), 371-377).

The amino acid sequence of the FlgE polypeptide has significant resemblance with
15 that of other known hook proteins, including limited homology to other *Helicobacter* species like *mustelae* (O'Toole et al., *supra*). Polyclonal antibodies raised against the FlgE polypeptide showed cross-reactivity against flagellar proteins A and B, possibly indicating the existence of shared epitopes. Production of FlgE knockout *H. pylori*, resulted in an aflagellar, non-motile bacteria, where FlgE
20 polypeptide still was produced but could only be recovered in the cytoplasm.

BRIEF DESCRIPTION OF THE DRAWINGS

25 Fig. 1:

Effect of therapeutic immunization of *H. pylori* infected mice (n=9-10/group) with FlgE polypeptide. Results are given as mean \pm SEM of number of *H. pylori* associated with antrum (=A), corpus (=B) or totally (A+C) (=C). Abbreviations: CFU, colony forming units (number of bacteria); unshaded bars=DOC + CT,
30 Phosphate buffered saline with 0.5% deoxycholate given together with cholera

toxin 10 µg/mouse; shaded bars=FlgE + CT, mice given 100 µg FlgE and 10 µg cholera toxin. The decrease in cfu was significant in the antrum and as calculated for the whole stomach.

** p<0.01; * p<0.05 (Wilcoxon-Mann-Whittney sign rank test).

5

Fig. 2:

Serum IgG from mice measured by ELISA technique: response to infection and to immunisation with FlgE. The values are expressed as mean titers ± SEM. n=9-10/group. ELISA coated with *H. pylori* strain 244: As a sign of infection *H. pylori* specific antibodies can be found in serum in animals treated with DOC + CT (=A. Control/244). Following immunization with FlgE + cholera toxin (=B. FlgE/244) this reactivity increased 4 fold (** p<0.01; Wilcoxon-Mann-Whittney sign rank test). C=FlgE specific. Specific FlgE IgG increased in animals given FlgE + CT, but could not be detected in control animals.

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DISCLOSURE OF THE INVENTION

The purpose of this invention is to provide an antigenic *H. pylori* polypeptide which can be useful for eliciting a protective immune response against, and for diagnosis of, *H. pylori* infection. This purpose has been achieved by the recombinant cloning of an *H. pylori* gene which encodes a well conserved essential polypeptide. The nucleic acid sequence of this gene is similar to the sequence of the *flgE* gene as published by O'Toole et al., Molecular Microbiology, 14(4), 691-703, 1994. Being an essential protein for motility, the *flgE* gene is expressed by all *H. pylori* strains.

It has surprisingly been found that the *H. pylori* FlgE polypeptide, in spite of the facts that only a small part of the hook protein is existing outside bacteria and that it is probably covered by a sheet, can serve as a therapeutic antigen in an *H. pylori*

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toxin 10 µg/mouse; shaded bars=FlgE + CT, mice given 100 µg FlgE and 10 µg cholera toxin. The decrease in cfu was significant in the antrum and as calculated for the whole stomach.

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to identify modified forms of the FlgE polypeptide retaining functionally equivalent antigenicity, by use of known methods, such as epitope mapping with *in vivo* induced antibodies.

- 5 In a preferred form of the invention, the *Helicobacter pylori* FlgE polypeptide, for use in inducing a protective immune response to *Helicobacter pylori* infection, has substantially the amino acid sequence set forth as SEQ ID NO: 2 in the Sequence Listing, or is a modified form thereof retaining functionally equivalent antigenicity.

- 10 It is thus to be understood that the definition of the *Helicobacter pylori* FlgE polypeptide is not to be limited strictly to a polypeptide with an amino acid sequence identical with SEQ ID NO: 2 in the Sequence Listing. Rather the invention encompasses polypeptides carrying modifications like substitutions,
15 small deletions, insertions or inversions, which polypeptides nevertheless have substantially the biological activities of the *Helicobacter pylori* FlgE polypeptide and is retaining functionally equivalent antigenicity. Included in the definition of the *Helicobacter pylori* FlgE polypeptide are consequently polypeptides, the amino acid sequence of which is at least 90% homologous, preferably at least 95%
20 homologous, with the amino acid sequence set forth as SEQ ID NO: 2 in the Sequence Listing.

- In another aspect, the invention provides a vaccine composition for inducing a protective immune response to *Helicobacter pylori* infection, comprising an
25 immunogenically effective amount of a *Helicobacter pylori* FlgE polypeptide as defined above, optionally together with a pharmaceutically acceptable carrier or diluent.

- In the present context the term "immunologically effective amount" is to be
30 understood as an amount which elicits a significant protective *Helicobacter pylori*

response, which will eradicate a *H. pylori* infection in an infected mammal or prevent the infection in a susceptible mammal. Typically an immunologically effective amount will comprise approximately 1 µg to 1000 mg, preferably approximately 10 µg to 100 mg, of *H. pylori* antigen for oral administration, or
5 approximately less than 100 µg for parenteral administration.

The vaccine composition comprises optionally in addition to a pharmaceutically acceptable carrier or diluent one or more other immunologically active antigens for prophylactic or therapeutic use. Physiologically acceptable carriers and
10 diluents are well known to those skilled in the art and include e.g. phosphate buffered saline (PBS), or, in the case of oral vaccines, HCO₃⁻ based formulations or enterically coated powder formulations.

The vaccine composition can optionally include or be administered together with
15 acid secretion inhibitors, preferably proton pump inhibitors (PPIs), e.g. omeprazole. The vaccine can be formulated in known delivery systems such as liposomes, ISCOMs, cochleates, etc. (see e.g. Rabinovich et al. (1994) Science 265, 1401-1404) or be attached to or incorporated into polymer microspheres of degradable or non-degradable nature. The antigens could be associated with live
20 attenuated bacteria, viruses or phages or with killed vectors of the same kind. The antigens can be chemically or genetically coupled to carrier proteins of inert or adjuvant types (i.e. Cholera B subunit). Consequently, the invention provides in a further aspect a vaccine composition according to above, in addition comprising an adjuvant, such as a cholera toxin. Such pharmaceutically acceptable forms of
25 cholera toxin are known in the art, e.g. from Rappuoli et al. (1995) Int. Arch. Allergy & Immunol. 108(4), 327-333; and Dickinson et al. (1995) Infection and Immunity 63(5), 1617-1623.

A vaccine composition according to the invention can be used for both therapeutic
30 and prophylactic purposes. Consequently, the invention includes a vaccine

composition according as defined above, for use as a therapeutic or a prophylactic vaccine in a mammal, including man, which is infected by *Helicobacter pylori*. In this context the term "prophylactic purpose" means to induce an immune response which will protect against future infection by *Helicobacter pylori*, while
5 the term "therapeutic purpose" means to induce an immune response which can eradicate an existing *Helicobacter pylori* infections.

The vaccine composition according to the invention is preferably administered to any mammalian mucosa exemplified by the buccal, the nasal, the tonsillar, the
10 gastric, the intestinal (small and large intestine), the rectal and the vaginal mucosa. The mucosal vaccines can be given together with for the purpose appropriate adjuvants. The vaccine can also be given orally, or parenterally, by the subcutaneous, intracutaneous or intramuscular route, optionally together with the appropriate adjuvant. The vaccine composition can optionally be given together
15 with antimicrobial therapeutic agents.

In a further aspect, the invention provides the use of a *Helicobacter pylori* FlgE polypeptide, as defined above, in the manufacture of
(i) a composition for the treatment, prophylaxis or diagnosis of *Helicobacter pylori*
20 infection;
(ii) a vaccine for use in eliciting a protective immune response against *Helicobacter pylori*; and
(iii) a diagnostic kit for diagnosis of *Helicobacter pylori* infection.

25 In yet a further aspect, the invention provides a method of *in vitro* diagnosis of *Helicobacter pylori* infection comprising at least one step wherein a *Helicobacter pylori* FlgE polypeptide as defined above, optionally labelled or coupled to a solid support, is used. The said method could e.g. comprise the steps (a) contacting a said *Helicobacter pylori* FlgE polypeptide, optionally bound to a solid support, with

a body fluid taken from a mammal; and (b) detecting antibodies from the said body fluid binding to the said FlgE polypeptide. Preferred methods of detecting antibodies are ELISA (Enzyme linked immunoabsorbent assay) methods which are well known in the art.

5

In another aspect the invention provides a diagnostic kit for the detection of *Helicobacter pylori* infection in a mammal, including man, comprising components which enable the method of *in vitro* diagnosis as described above to be carried out. The said diagnostic kit could e.g. comprise: (a) a *Helicobacter pylori* FlgE polypeptide; and (b) reagents for detecting antibodies binding to the said FlgE polypeptide. The said reagents for detecting antibodies could e.g. be an enzyme-labelled anti-immunoglobulin and a chromogenic substrate for the said enzyme.

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In yet a further aspect, the invention provides a method of eliciting in a mammal, including humans, a protective immune response against *Helicobacter pylori* infection, said method comprising the step of administering to the said mammal an immunologically effective amount of a *Helicobacter pylori* FlgE polypeptide as defined above, or alternatively administering to the said mammal an immunologically effective amount of a vaccine composition as defined above.

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EXPERIMENTAL METHODS

Throughout this description the terms "standard protocols" and "standard procedures", when used in the context of molecular cloning techniques, are to be understood as protocols and procedures found in an ordinary laboratory manual such as: Current Protocols in Molecular Biology, editors F. Ausubel et al., John Wiley and Sons, Inc. 1994, or Sambrook, J., Fritsch, E.F. and Maniatis, T., Molecular Cloning: A laboratory manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY 1989.

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Preparation of recombinant Helicobacter pylori FlgE polypeptide

DNA sequence Information

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Sequence information for the gene encoding for the FlgE polypeptide was obtained from the National Center for Biotechnology Information (Accession number U09549; SEQ ID NO: 1).

- 10 *PCR Amplification and cloning of DNA sequences containing ORF's for membrane and secreted proteins from the J99 Strain of Helicobacter pylori.*

Sequences were cloned from the J99 strain of *H. pylori* by amplification cloning using the polymerase chain reaction (PCR). Synthetic oligonucleotide primers (see
15 below) specific for the 5'- and 3'-ends of open reading frames of genes were designed and purchased (GibcoBRL Life Technologies, Gaithersburg, MD, USA). Forward primers (specific for the 5'-end of the sequence) for FlgE were designed to include an *NcoI* cloning site at the extreme 5'-terminus, while reverse primers included a *EcoRI* site at the extreme 5'-terminus to permit cloning of each *H. pylori*
20 sequence into the reading frame of the pET28b vector. Inserts cloned into the *NcoI*-*EcoRI* sites of the pET-28b vector are fused to a vector DNA sequence encoding an additional 20 carboxy-terminal amino including six histidine residues (at the extreme C-terminus).

- 25 Forward primer (SEQ ID NO: 3):
5'-TAT ACC ATG GTG CTT AGG TCT TTA T-3'
Reverse primer (SEQ ID NO: 4):
5'-GCG AAT TCA ATT GCT TAA GAT TCA A-3'

Genomic DNA prepared from the J99 strain of *Helicobacter pylori* was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, editors F. Ausubel et al., John Wiley and Sons, Inc. 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (50 ng) was
5 introduced into a reaction vial containing 2 mM MgCl₂, 1 μM synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate dATP, dGTP, dCTP, dTTP, and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume
10 of 100 μl. The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:
Denaturation at +94°C for 2 min;
2 cycles at +94°C for 15 sec, +30°C for 15 sec and +72°C for 1.5 min;
15 23 cycles at +94°C for 15 sec, +58°C for 15 sec and +72°C for 1.5 min;
Reactions were concluded at +72°C for 6 minutes.

Upon completion of thermal cycling reactions, each sample of amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen,
20 Gaithersburg, MD, USA). Amplified DNA samples were subjected to digestion with the restriction endonucleases *NdeI* and *EcoRI* according to standard procedures. DNA samples were then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA was visualized by exposure to ethidium bromide and long wave UV irradiation. DNA
25 contained in slices isolated from the agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

Cloning of H. pylori DNA sequences into the pET-28b prokaryotic expression vector.

The pET-28b vector was prepared for cloning by digestion with *Nco*I and *Eco*RI according to standard procedures. Following digestion, DNA inserts were cloned
5 according to standard procedures into the previously digested pET-28b expression vector. Products of the ligation reaction were then used to transform the BL21 strain of *E. coli* as described below.

Transformation of competent bacteria with recombinant plasmids

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Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), were transformed with recombinant pET expression plasmids carrying the cloned *H. pylori* sequences according to standard methods. Briefly, 1 µl of ligation reaction was mixed with 50 µl of electrocompetent cells and subjected to a high voltage
15 pulse, after which, samples were incubated in 0.45 ml SOC medium (0.5% yeast extract, 2.0% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at +37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 µg/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 were then picked and analyzed to evaluate cloned
20 inserts as described below.

Identification of recombinant pET expression plasmids carrying H. pylori sequences

Individual BL21 clones transformed with recombinant pET-28b *H. pylori* genes
25 were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the expression vector according to standard procedures.

Isolation and Preparation of plasmid DNA from BL21 transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *H. pylori* ORFs were picked and incubated in 5 ml of LB broth plus 25 µg/ml kanamycin sulfate overnight. The following day plasmid DNA was isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

10 *Expression of recombinant H. pylori sequences in E. coli*

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5α, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the *lacI* gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-β-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used in our laboratory include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Methods Enzymol. 185, 60-89).

To express recombinant *H. pylori* sequences, 50 ng of plasmid DNA isolated as described above was used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). Transformed cells were cultured in SOC medium for 1 hour, and the culture was then plated on LB plates containing 25 µg/ml kanamycin sulfate. The following day, bacterial colonies were pooled and grown in LB medium containing kanamycin sulfate (25 µg/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D.

units, at which point, 1 mM IPTG was added to the culture for 3 hours to induce gene expression of the *H. pylori* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria were pelleted by
5 centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets were resuspended in 50 ml cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells were then centrifuged at 2000 x g for 20 min at +4°C. Wet pellets were weighed and frozen at -80°C until ready for protein purification.

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Analytical Methods

The concentrations of purified protein preparations were quantified spectrophotometrically using absorbance coefficients calculated from amino acid
15 content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations were also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) , using bovine serum albumin as a standard.

20 Sodium dodecyl sulfate-polyacrylamide (SDS-PAGE) gels (12% or 4 to 25 % gradient acrylamide) were purchased from BioRad (Hercules, CA, USA), and stained with Coomassie Brilliant Blue. Molecular mass markers included rabbit skeletal muscle myosin (200 kDa), *E. coli* β -galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45
25 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

Purification of FlgE from inclusion bodies

The following steps were carried out at +4°C. Cell pellets were resuspended in lysis buffer with 10% glycerol 200 µg/ml lysozyme, 5 mM EDTA, 1 mM PMSF and
5 0.1% β-mercaptoethanol. After passage through the cell disrupter, the resulting homogenate was made 0.2% DOC, stirred 10 minutes, then centrifuged (10,000 g x 30 min). The pellets were first washed with lysis buffer containing 10% glycerol, 10 mM EDTA, 1% Triton X-100, 1 mM PMSF and 0.1% β-mercaptoethanol, then with lysis buffer containing 1 M urea, 1 mM PMSF and 0.1% β-mercaptoethanol. The
10 resulting white pellet was composed primarily of inclusion bodies, free of unbroken cells and membranous materials.

The following steps were carried out at room temperature. Inclusion bodies were dissolved in 20 ml 8 M urea in lysis buffer with 1 mM PMSF and 0.1% β-
15 mercaptoethanol, and incubated at room temperature for 1 hour. Materials that did not dissolve were removed by centrifugation (100,000 x g for 30 min) . The clear supernatant was filtered and loaded onto a Ni²⁺-NTA agarose column equilibrated in 8 M urea in lysis buffer. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 8 M urea, 1 mM PMSF and 0.1% β-
20 mercaptoethanol, and developed with sequential steps of lysis buffer containing 8 M urea, 1 mM PMSF, 0.1% β-mercaptoethanol and 20, 100, 200, and 500 mM imidazole. Fractions were monitored by absorbance at OD₂₈₀ nm, and peak fractions were analyzed by SDS-PAGE. Two bands were visualized by Coomassie Brilliant Blue staining, a major band M_r = 78 kDa and a minor band M_r = 60 kDa.
25 Purity of recombinant FlgE (78 kDa) was assessed at greater than 90%. As with the purification of the soluble proteins, fractions containing the recombinant protein eluted at 100 mM imidazole.

Urea was slowly removed from the FlgE polypeptide by dialysis against TBS
30 containing 0.5% DOC with sequential reduction in urea as follows; 6M, 4M, 3M,

2M, 1M, 0.5 M then 0 M. Each dialysis step was carried for a minimum of 4 hours at room temperature,

After dialysis, samples were concentrated by pressure filtration using Amicon stirred cells. Protein concentrations were then measured by the methods of Perkins, Bradford and Lowry.

EXAMPLES OF THE INVENTION

EXAMPLE 1: THERAPEUTIC IMMUNIZATION

1. Materials & Methods

1.1 Animals

Female SPF BALB/c mice were purchased from Bomholt Breeding centre (Denmark). They were kept in ordinary makrolon cages with free supply of water and food. The animals were 4-6 weeks old at arrival.

1.2. Infection

After a minimum of one week of acclimatization, the animals were infected with a type 2 strain of *H. pylori* (strain 244, originally isolated from an ulcer patient). This strain has earlier proven to be a good colonizer of the mouse stomach. Bacteria from a stock kept at -70°C were grown overnight in Brucella broth supplemented with 10% fetal calf serum, at +37°C in a microaerophilic atmosphere (10% CO₂, 5% O₂). The animals were given an oral dose of omeprazole (400 µmol/kg) and after 3-5 h an oral inoculation of *H. pylori* (approximately 10⁷-10⁸ CFU/animal).

Infection was checked in control animals 2-3 weeks after the inoculation.

1.3. Immunizations

One month after infection, two groups of mice (10 mice/group) were immunized 4 times over a 34 day period (day 1, 15, 25 and 35). Purified recombinant FlgE
5 dissolved in PBS plus 0.5% Deoxycholate (DOC) was given at a dose of 100 microgram/mouse.

As an adjuvant, the animals in both the control as well as the FlgE group were also given 10 µg/mouse of cholera toxin (CT) with each immunization. Omeprazole
10 (400 µmol/kg) was given orally to all animals 3-5 h prior to immunization as a way of protecting the antigens from acid degradation. Animals were sacrificed 1-2 weeks after final immunization.

Group 1: 300 µl PBS with 0.5% DOC containing 10 µg CT

Group 2: 300 µl PBS with 0.5% DOC containing 100 µg FlgE and 10 µg CT.

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1.4. Analysis of infection

The mice were sacrificed by CO₂ and cervical dislocation. The abdomen and chest cavity was opened and blood sampled by heart puncture. Subsequently the
20 stomach was removed. After cutting the stomach along the greater curvature, it was rinsed in saline and subsequently cut into two identical pieces. An area of 25 mm² of the mucosa from the antrum and corpus was scraped separately with a surgical scalpel. The mucosa scraping was suspended in Brucella broth, diluted and plated onto Blood Skirrow plates. The plates were incubated under
25 microaerophilic conditions for 3-5 days and the number of colonies was counted. The identity of *H. pylori* was ascertained by urease and catalase test and by direct microscopy or Gram staining.

1.5. Antibody measurements

Serum antibodies were collected from blood. Prior to centrifugation, the blood was diluted with equal amount of PBS. The serum was kept at -20°C until analysis.

- 5 Serum antibodies were measured using an ELISA where plates were coated either with a particulate fraction of *H. pylori* strain 244 or with FlgE followed by addition of different dilutions of serum. The ELISA was developed with alkaline phosphatase-labelled anti-mouse-Ig-antibodies. The anti-Ig antibodies were of an anti-heavy /anti-light chain type, which should detect all types of antibodies.

10

2. Results

2.1. Therapeutic immunization: effects on CFU

- 15 The animals in this study were infected with *H. pylori* strain 244 one month prior to immunizations. Mice in groups of ten were then immunized with either cholera toxin (CT) or CT together with the recombinant FlgE polypeptide. Four weeks after the final immunization, the animals were sacrificed and CFU was determined (Fig. 1). The animals treated with CT alone, were highly infected both in corpus
20 and antrum. Animals actively immunized with recombinant FlgE polypeptide and CT had significantly decreased CFU values in the antrum and in the stomach as a whole compared with the CT treated animals ($p<0.01$ and $p<0.05$, respectively; Wilcoxon-Mann-Whittney sign rank test).

- 25 2.2. Therapeutic immunization: effects on antibody formation and secretion

As a sign of infection *H. pylori* specific antibodies can be found in serum (Control/244). In animals given FlgE + CT the titer against strain 244 (as membrane proteins) increased 4-fold ($p<0.01$). Only in animals given FlgE + CT
30 could a specific serum IgG titer against FlgE be measured (Fig. 2).

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Astra AB
(B) STREET: Västra Mälarehamnen 9
(C) CITY: Södertälje
(E) COUNTRY: Sweden
(F) POSTAL CODE (ZIP): S-151 85
(G) TELEPHONE: +46 8 553 260 00
(H) TELEFAX: +46 8 553 288 20

(ii) TITLE OF INVENTION: Vaccine Compositions V

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 321..2477
(D) OTHER INFORMATION: /product= "FlgE flagellar hook protein"

(x) PUBLICATION INFORMATION:

(A) AUTHORS: O'Toole, Paul W.
Kostrzynska, Magdalena
Trust, Trevor J.
(B) TITLE: Non-motile mutants of Helicobacter pylori and
Helicobacter mustelae defective in flagellar hook
production
(C) JOURNAL: Mol. Microbiol.
(D) VOLUME: 14
(E) ISSUE: 4
(F) PAGES: 691-703
(G) DATE: 1994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AACAAAGCGA TAACTCCTTT GTCTTATTAG CGACACAATT TAACCCATTG ACTTTAAATC	60
GCGCTTCAGC CGAAGAGATT CAAGATCATG AATGCGCGAT TTTGCACTAA AGCGAGTTAG	120
ATTCTTAAAT TTGAGCGATA ACCTTTAAAA AGCGTAATTA AGGGGTGGTG TTACAAAACC	180

CCCTATCCCC TTATGAATTT GACCGATCTT TTTGATTAAC AAAACTTTAA AATCCGCAAT	240
CAATCATTCT AAAAAGCTAT TTAGGAACAA CTTTGTCTTT ATTTTGCATA GATTGAATTT	300
CTTTAAATTA AAGGATAACC ATG CTT AGG TCT TTA TGG TCT GGT GTC AAT Met Leu Arg Ser Leu Trp Ser Gly Val Asn 1 5 10	350
GGG ATG CAA GCC CAC CAA ATC GCT TTG GAT ATT GAG AGT AAC AAT ATT Gly Met Gln Ala His Gln Ile Ala Leu Asp Ile Glu Ser Asn Asn Ile 15 20 25	398
GCG AAC GTG AAT ACC ACT GGT TTT AAG TAT TCT AGG GCT TCT TTT GTG Ala Asn Val Asn Thr Thr Gly Phe Lys Tyr Ser Arg Ala Ser Phe Val 30 35 40	446
GAT ATG CTT TCT CAA GTC AAA CTC ATC GCT ACC GCA CCC TAT AAA AAC Asp Met Leu Ser Gln Val Lys Leu Ile Ala Thr Ala Pro Tyr Lys Asn 45 50 55	494
GGG TTA GCA GGG CAG AAT GAT TTT TCT GTG GGG CTT GGG GTA GGC GTG Gly Leu Ala Gly Gln Asn Asp Phe Ser Val Gly Leu Gly Val Gly Val 60 65 70	542
GAT GCG ACG ACT AAA ATC TTT TCA CAA GGC AAT ATC CAA AAC ACA GAT Asp Ala Thr Thr Lys Ile Phe Ser Gln Gly Asn Ile Gln Asn Thr Asp 75 80 85 90	590
GTC AAA ACC GAT CTA GCG ATT CAA GGC GAT GGC TTT TTT ATC ATT AAC Val Lys Thr Asp Leu Ala Ile Gln Gly Asp Gly Phe Phe Ile Ile Asn 95 100 105	638
CCT GAT AGG GGG ATC ACG CGC AAT TTC ACT AGA GAT GGG GAG TTC CTT Pro Asp Arg Gly Ile Thr Arg Asn Phe Thr Arg Asp Gly Glu Phe Leu 110 115 120	686
TTT GAC TCG CAA GGG AGT TTG GTT ACC ACC GGC GGG CTT GTG GTG CAA Phe Asp Ser Gln Gly Ser Leu Val Thr Thr Gly Gly Leu Val Val Gln 125 130 135	734
GGG TGG GTG AGA AAT GGG AGC GAT ACC GGC AAT AAA GGG AGC GAT ACA Gly Trp Val Arg Asn Gly Ser Asp Thr Gly Asn Lys Gly Ser Asp Thr 140 145 150	782
GAC GCT TTA AAA GTG GAT AAC ACC GGT CCT TTA GAA AAC ATT AGG ATT Asp Ala Leu Lys Val Asp Asn Thr Gly Pro Leu Glu Asn Ile Arg Ile 155 160 165 170	830
GAT CCT GGA ATG GTG ATG CCA GCC AGA GCG AGT AAC CGC ATT TCT ATG Asp Pro Gly Met Val Met Pro Ala Arg Ala Ser Asn Arg Ile Ser Met 175 180 185	878
AGG GCG AAT TTA AAC GCT GGA AGG CAT GCC GAT CAA ACA GCG GCG ATA Arg Ala Asn Leu Asn Ala Gly Arg His Ala Asp Gln Thr Ala Ala Ile 190 195 200	926
TTC GCT TTG GAT TCT TCA GCC AAA ACC CCT TCA GAT GGC ATT AAT CCG Phe Ala Leu Asp Ser Ser Ala Lys Thr Pro Ser Asp Gly Ile Asn Pro 205 210 215	974
GTG TAT GAT TCA GGC ACG AAT CTT GCT CAA GTC GCC GAA GAC ATG GGA Val Tyr Asp Ser Gly Thr Asn Leu Ala Gln Val Ala Glu Asp Met Gly 220 225 230	1022
TCT TTA TAC AAT GAA GAT GGC GAC GCT CTT TTG TTG AAT GAA AAT CAA	1070

Ser 235	Leu	Tyr	Asn	Glu	Asp 240	Gly	Asp	Ala	Leu	Leu 245	Leu	Asn	Glu	Asn	Gln 250		
GGG Gly	ATT Ile	TGG Trp	GTG Val	AGC Ser	TAT Tyr	AAG Lys	AGT Ser	CCA Pro	AAA Lys	ATG Met	GTC Val	AAA Lys	GAC Asp	ATC Ile	CTC Leu	1118	
CCT Pro	TCT Ser	GCA Ala	GAA Glu	AAC Asn	AGC Ser	ACG Thr	CTT Leu	GAA Glu	TTG Leu	AAT Asn	GGC Gly	GTT Val	AAG Lys	ATT Ile	TCT Ser	1166	
TTC Phe	ACA Thr	AAC Asn	GAT Asp	TCA Ser	GCG Ala	GTG Val	AGC Ser	CGG Arg	ACT Thr	TCA Ser	AGC Ser	TTA Leu	GTG Val	GCG Ala	GCT Ala	1214	
AAA Lys	AAT Asn	GCG Ala	ATC Ile	AAT Asn	GCA Ala	GTC Val	AAA Lys	AGC Ser	CAA Gln	ACA Thr	GGC Gly	ATT Ile	GAA Glu	GCT Ala	TAT Tyr	1262	
TTA Leu	GAC Asp	GGC Gly	AAG Lys	CAA Gln	TTG Leu	CGT Arg	TTG Leu	GAA Glu	AAC Asn	ACC Thr	AAT Asn	GAA Glu	TTA Leu	GAC Asp	GGC Gly	1310	
GAT Asp	GAA Glu	AAG Lys	CTT Leu	AAA Lys	AAC Asn	ATT Ile	GTA Val	GTT Val	ACT Thr	CAA Gln	GCC Ala	GGA Gly	ACC Thr	GGA Gly	GCG Ala	1358	
TTC Phe	GCT Ala	AAC Asn	TTT Phe	TTA Leu	GAC Asp	GGC Gly	GAT Asp	AAA Lys	GAT Asp	GTA Val	ACG Thr	GCT Ala	TTT Phe	AAA Lys	TAC Tyr	1406	
AGC Ser	TAC Tyr	ACG Thr	CAT His	TCT Ser	ATT Ile	AGC Ser	CCT Pro	AAC Asn	GCC Ala	AAT Asn	AGC Ser	GGG Gly	CAG Gln	TTT Phe	AGG Arg	1454	
ACC Thr	ACT Thr	GAA Glu	GAC Asp	TTG Leu	CGC Arg	GCC Ala	TTA Leu	ATC Ile	CAG Gln	CAT His	GAC Asp	GCT Ala	AAT Asn	ATC Ile	GTT Val	1502	
AAA Lys	GAT Asp	CCT Pro	AGC Ser	CTA Leu	GCG Ala	GAC Asp	AAT Asn	TAC Tyr	CAA Gln	GAC Asp	TCA Ser	GCC Ala	GCT Ala	TCT Ser	ATA Ile	1550	
GGA Gly	GTT Val	ACA Thr	ATC Ile	AAC Asn	CAA Gln	TAC Tyr	GGC Gly	ATG Met	TTT Phe	GAA Glu	ATC Ile	AAC Asn	AAT Asn	AAA Lys	GAC Asp	1598	
AAT Asn	AAA Lys	AAT Asn	GTC Val	ATT Ile	AAA Lys	GAA Glu	AAT Asn	CTT Leu	AAT Asn	ATC Ile	TTT Phe	GTG Val	AGC Ser	GGG Gly	TAT Tyr	1646	
TCT Ser	TCA Ser	GAC Asp	AGC Ser	GTA Val	ACG Thr	AAC Asn	AAT Asn	GTT Val	TTG Leu	TTT Phe	AAA Lys	AAT Asn	GCG Ala	ATG Met	AAA Lys	1694	
GGG Gly	CTT Leu	AAT Asn	ACC Thr	GCT Ala	TCT Ser	TTA Leu	ATT Ile	GAA Glu	GGG Gly	GGA Gly	GCG Ala	TCA Ser	GCG Ala	AGC Ser	AGT Ser	1742	
TCT Ser	AAA Lys	TTC Phe	ACC Thr	CAC His	GCT Ala	ACG Thr	CAT His	GCG Ala	ACA Thr	AGC Ser	ATT Ile	GAT Asp	GTG Val	ATA Ile	GAC Asp	1790	
AGC Ser	TTA Leu	GGC Gly	ACT Thr	AAA Lys	CAC His	GCC Ala	ATG Met	CGC Arg	ATT Ile	GAG Glu	TTT Phe	TAT Tyr	AGG Arg	AGT Ser	GGG Gly	1838	

GGA GCG GAT TGG AAT TTT AGA GTG ATC GTG CCT GAG CCT GGG GAA TTA Gly Ala Asp Trp Asn Phe Arg Val Ile Val Pro Glu Pro Gly Glu Leu 510 515 520	1886
GTA GGG GGG TCA GCG GCT AGG CCT AAT GTG TTT GAA GGA GGC CGT TTG Val Gly Gly Ser Ala Ala Arg Pro Asn Val Phe Glu Gly Gly Arg Leu 525 530 535	1934
CAC TTC AAT AAT GAC GGA TCG CTT GCA GGC ATG AAC CCG CCT CTT TTG His Phe Asn Asn Asp Gly Ser Leu Ala Gly Met Asn Pro Pro Leu Leu 540 545 550	1982
CAA TTT GAC CCT AAA AAT GGT GCT GAT GCC CCC CAA CGC ATC AAT TTA Gln Phe Asp Pro Lys Asn Gly Ala Asp Ala Pro Gln Arg Ile Asn Leu 555 560 565 570	2030
GCT TTT GGT TCC TCA GGG AGT TTT GAC GGG CTA ACG AGC GTG GAT AAG Ala Phe Gly Ser Ser Gly Ser Phe Asp Gly Leu Thr Ser Val Asp Lys 575 580 585	2078
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TTG ATG GAT GTC CGC TTT GAT TCA GAT GGG GTG CTT TTA GGA GCG TTC Leu Met Asp Val Arg Phe Asp Ser Asp Gly Val Leu Leu Gly Ala Phe 605 610 615	2174
AGT AAT GGC AGG ACT TTA GCG CTC GCT CAA GTG GCT TTA GCG AAT TTC Ser Asn Gly Arg Thr Leu Ala Leu Ala Gln Val Ala Leu Ala Asn Phe 620 625 630	2222
GCT AAC GAT GCG GGC TTG CAG GCT TTA GGC GGG AAT GTC TTT TCT CAA Ala Asn Asp Ala Gly Leu Gln Ala Leu Gly Gly Asn Val Phe Ser Gln 635 640 645 650	2270
ACC GGA AAC TCA GGG CAA GCC TTA ATC GGT GCG GCT AAT ACG GGG CGT Thr Gly Asn Ser Gly Gln Ala Leu Ile Gly Ala Ala Asn Thr Gly Arg 655 660 665	2318
AGG GGT TCA ATT TCA GGA TCT AAA CTG GAG TCT AGT AAT GTG GAT TTG Arg Gly Ser Ile Ser Gly Ser Lys Leu Glu Ser Ser Asn Val Asp Leu 670 675 680	2366
AGC CGG AGT TTA ACG AAT TTG ATT GTG GTT CAA AGG GGC TTT CAA GCA Ser Arg Ser Leu Thr Asn Leu Ile Val Val Gln Arg Gly Phe Gln Ala 685 690 695	2414
AAC TCT AAA GCG GTA ACC ACA TCC GAT CAA ATC CTT AAT ACC CTA TTG Asn Ser Lys Ala Val Thr Thr Ser Asp Gln Ile Leu Asn Thr Leu Leu 700 705 710	2462
AAT CTT AAG CAA TAA ACTAAAGGAT TACTCTAATA CAATATAATA GGGGCTAATT Asn Leu Lys Gln * 715	2517
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(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 719 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

GGA GCG GAT TGG AAT TTT AGA GTG ATC GTG CCT GAG CCT GGG GAA TTA Gly Ala Asp Trp Asn Phe Arg Val Ile Val Pro Glu Pro Gly Glu Leu 510 515 520	1886
GTA GGG GGG TCA GCG GCT AGG CCT AAT GTG TTT GAA GGA GGC CGT TTG Val Gly Gly Ser Ala Ala Arg Pro Asn Val Phe Glu Gly Gly Arg Leu 525 530 535	1934
CAC TTC AAT AAT GAC GGA TCG CTT GCA GGC ATG AAC CCG CCT CTT TTG His Phe Asn Asn Asp Gly Ser Leu Ala Gly Met Asn Pro Pro Leu Leu 540 545 550	1982
CAA TTT GAC CCT AAA AAT GGT GCT GAT GCC CCC CAA CGC ATC AAT TTA Gln Phe Asp Pro Lys Asn Gly Ala Asp Ala Pro Gln Arg Ile Asn Leu 555 560 565 570	2030
GCT TTT GGT TCC TCA GGG AGT TTT GAC GGG CTA ACG AGC GTG GAT AAG Ala Phe Gly Ser Ser Gly Ser Phe Asp Gly Leu Thr Ser Val Asp Lys 575 580 585	2078
ATT TCT GAA ACT TAT GCG ATT GAG CAA AAC GGC TAT CAA GCG GGC GAT Ile Ser Glu Thr Tyr Ala Ile Glu Gln Asn Gly Tyr Gln Ala Gly Asp 590 595 600	2126
TTG ATG GAT GTC CGC TTT GAT TCA GAT GGG GTG CTT TTA GGA GCG TTC Leu Met Asp Val Arg Phe Asp Ser Asp Gly Val Leu Leu Gly Ala Phe 605 610 615	2174
AGT AAT GGC AGG ACT TTA GCG CTC GCT CAA GTG GCT TTA GCG AAT TTC Ser Asn Gly Arg Thr Leu Ala Leu Ala Gln Val Ala Leu Ala Asn Phe 620 625 630	2222
GCT AAC GAT GCG GGC TTG CAG GCT TTA GGC GGG AAT GTC TTT TCT CAA Ala Asn Asp Ala Gly Leu Gln Ala Leu Gly Gly Asn Val Phe Ser Gln 635 640 645 650	2270
ACC GGA AAC TCA GGG CAA GCC TTA ATC GGT GCG GCT AAT ACG GGG CGT Thr Gly Asn Ser Gly Gln Ala Leu Ile Gly Ala Ala Asn Thr Gly Arg 655 660 665	2318
AGG GGT TCA ATT TCA GGA TCT AAA CTG GAG TCT AGT AAT GTG GAT TTG Arg Gly Ser Ile Ser Gly Ser Lys Leu Glu Ser Ser Asn Val Asp Leu 670 675 680	2366
AGC CGG AGT TTA ACG AAT TTG ATT GTG GTT CAA AGG GGC TTT CAA GCA Ser Arg Ser Leu Thr Asn Leu Ile Val Val Gln Arg Gly Phe Gln Ala 685 690 695	2414
AAC TCT AAA GCG GTA ACC ACA TCC GAT CAA ATC CTT AAT ACC CTA TTG Asn Ser Lys Ala Val Thr Thr Ser Asp Gln Ile Leu Asn Thr Leu Leu 700 705 710	2462
AAT CTT AAG CAA TAA ACTAAAGGAT TACTCTAATA CAATATAATA GGGGCTAATT Asn Leu Lys Gln * 715	2517
TAAAGATTAA GGTTTAGTAT GCATGAATAC TCG	2550

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Arg Ser Leu Trp Ser Gly Val Asn Gly Met Gln Ala His Gln
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 20 25 30
 Gly Phe Lys Tyr Ser Arg Ala Ser Phe Val Asp Met Leu Ser Gln Val
 35 40 45
 Lys Leu Ile Ala Thr Ala Pro Tyr Lys Asn Gly Leu Ala Gly Gln Asn
 50 55 60
 Asp Phe Ser Val Gly Leu Gly Val Gly Val Asp Ala Thr Thr Lys Ile
 65 70 75 80
 Phe Ser Gln Gly Asn Ile Gln Asn Thr Asp Val Lys Thr Asp Leu Ala
 85 90 95
 Ile Gln Gly Asp Gly Phe Phe Ile Ile Asn Pro Asp Arg Gly Ile Thr
 100 105 110
 Arg Asn Phe Thr Arg Asp Gly Glu Phe Leu Phe Asp Ser Gln Gly Ser
 115 120 125
 Leu Val Thr Thr Gly Gly Leu Val Val Gln Gly Trp Val Arg Asn Gly
 130 135 140
 Ser Asp Thr Gly Asn Lys Gly Ser Asp Thr Asp Ala Leu Lys Val Asp
 145 150 155 160
 Asn Thr Gly Pro Leu Glu Asn Ile Arg Ile Asp Pro Gly Met Val Met
 165 170 175
 Pro Ala Arg Ala Ser Asn Arg Ile Ser Met Arg Ala Asn Leu Asn Ala
 180 185 190
 Gly Arg His Ala Asp Gln Thr Ala Ala Ile Phe Ala Leu Asp Ser Ser
 195 200 205
 Ala Lys Thr Pro Ser Asp Gly Ile Asn Pro Val Tyr Asp Ser Gly Thr
 210 215 220
 Asn Leu Ala Gln Val Ala Glu Asp Met Gly Ser Leu Tyr Asn Glu Asp
 225 230 235 240
 Gly Asp Ala Leu Leu Leu Asn Glu Asn Gln Gly Ile Trp Val Ser Tyr
 245 250 255
 Lys Ser Pro Lys Met Val Lys Asp Ile Leu Pro Ser Ala Glu Asn Ser
 260 265 270
 Thr Leu Glu Leu Asn Gly Val Lys Ile Ser Phe Thr Asn Asp Ser Ala
 275 280 285
 Val Ser Arg Thr Ser Ser Leu Val Ala Ala Lys Asn Ala Ile Asn Ala
 290 295 300
 Val Lys Ser Gln Thr Gly Ile Glu Ala Tyr Leu Asp Gly Lys Gln Leu
 305 310 315 320
 Arg Leu Glu Asn Thr Asn Glu Leu Asp Gly Asp Glu Lys Leu Lys Asn

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Leu Arg Ser Leu Trp Ser Gly Val Asn Gly Met Gln Ala His Gln
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          20           25           30
Gly Phe Lys Tyr Ser Arg Ala Ser Phe Val Asp Met Leu Ser Gln Val
          35           40           45
Lys Leu Ile Ala Thr Ala Pro Tyr Lys Asn Gly Leu Ala Gly Gln Asn
          50           55           60
Asp Phe Ser Val Gly Leu Gly Val Gly Val Asp Ala Thr Thr Lys Ile
          65           70           75           80
Phe Ser Gln Gly Asn Ile Gln Asn Thr Asp Val Lys Thr Asp Leu Ala
          85           90           95
Ile Gln Gly Asp Gly Phe Phe Ile Ile Asn Pro Asp Arg Gly Ile Thr
          100          105          110
Arg Asn Phe Thr Arg Asp Gly Glu Phe Leu Phe Asp Ser Gln Gly Ser
          115          120          125
Leu Val Thr Thr Gly Gly Leu Val Val Gln Gly Trp Val Arg Asn Gly
          130          135          140
Ser Asp Thr Gly Asn Lys Gly Ser Asp Thr Asp Ala Leu Lys Val Asp
          145          150          155          160
Asn Thr Gly Pro Leu Glu Asn Ile Arg Ile Asp Pro Gly Met Val Met
          165          170          175
Pro Ala Arg Ala Ser Asn Arg Ile Ser Met Arg Ala Asn Leu Asn Ala
          180          185          190
Gly Arg His Ala Asp Gln Thr Ala Ala Ile Phe Ala Leu Asp Ser Ser
          195          200          205
Ala Lys Thr Pro Ser Asp Gly Ile Asn Pro Val Tyr Asp Ser Gly Thr
          210          215          220
Asn Leu Ala Gln Val Ala Glu Asp Met Gly Ser Leu Tyr Asn Glu Asp
          225          230          235          240
Gly Asp Ala Leu Leu Leu Asn Glu Asn Gln Gly Ile Trp Val Ser Tyr
          245          250          255
Lys Ser Pro Lys Met Val Lys Asp Ile Leu Pro Ser Ala Glu Asn Ser
          260          265          270
Thr Leu Glu Leu Asn Gly Val Lys Ile Ser Phe Thr Asn Asp Ser Ala
          275          280          285
Val Ser Arg Thr Ser Ser Leu Val Ala Ala Lys Asn Ala Ile Asn Ala
          290          295          300
Val Lys Ser Gln Thr Gly Ile Glu Ala Tyr Leu Asp Gly Lys Gln Leu
          305          310          315          320
Arg Leu Glu Asn Thr Asn Glu Leu Asp Gly Asp Glu Lys Leu Lys Asn

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325										330					335				
Ile	Val	Val	Thr	Gln	Ala	Gly	Thr	Gly	Ala	Phe	Ala	Asn	Phe	Leu	Asp				
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Gly	Asp	Lys	Asp	Val	Thr	Ala	Phe	Lys	Tyr	Ser	Tyr	Thr	His	Ser	Ile				
		355					360					365							
Ser	Pro	Asn	Ala	Asn	Ser	Gly	Gln	Phe	Arg	Thr	Thr	Glu	Asp	Leu	Arg				
	370					375					380								
Ala	Leu	Ile	Gln	His	Asp	Ala	Asn	Ile	Val	Lys	Asp	Pro	Ser	Leu	Ala				
385					390					395					400				
Asp	Asn	Tyr	Gln	Asp	Ser	Ala	Ala	Ser	Ile	Gly	Val	Thr	Ile	Asn	Gln				
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Tyr	Gly	Met	Phe	Glu	Ile	Asn	Asn	Lys	Asp	Asn	Lys	Asn	Val	Ile	Lys				
			420					425					430						
Glu	Asn	Leu	Asn	Ile	Phe	Val	Ser	Gly	Tyr	Ser	Ser	Asp	Ser	Val	Thr				
		435					440					445							
Asn	Asn	Val	Leu	Phe	Lys	Asn	Ala	Met	Lys	Gly	Leu	Asn	Thr	Ala	Ser				
		450				455					460								
Leu	Ile	Glu	Gly	Gly	Ala	Ser	Ala	Ser	Ser	Ser	Lys	Phe	Thr	His	Ala				
465					470					475					480				
Thr	His	Ala	Thr	Ser	Ile	Asp	Val	Ile	Asp	Ser	Leu	Gly	Thr	Lys	His				
				485					490					495					
Ala	Met	Arg	Ile	Glu	Phe	Tyr	Arg	Ser	Gly	Gly	Ala	Asp	Trp	Asn	Phe				
			500					505					510						
Arg	Val	Ile	Val	Pro	Glu	Pro	Gly	Glu	Leu	Val	Gly	Gly	Ser	Ala	Ala				
		515					520					525							
Arg	Pro	Asn	Val	Phe	Glu	Gly	Gly	Arg	Leu	His	Phe	Asn	Asn	Asp	Gly				
	530					535					540								
Ser	Leu	Ala	Gly	Met	Asn	Pro	Pro	Leu	Leu	Gln	Phe	Asp	Pro	Lys	Asn				
545					550					555					560				
Gly	Ala	Asp	Ala	Pro	Gln	Arg	Ile	Asn	Leu	Ala	Phe	Gly	Ser	Ser	Gly				
				565				570						575					
Ser	Phe	Asp	Gly	Leu	Thr	Ser	Val	Asp	Lys	Ile	Ser	Glu	Thr	Tyr	Ala				
			580					585					590						
Ile	Glu	Gln	Asn	Gly	Tyr	Gln	Ala	Gly	Asp	Leu	Met	Asp	Val	Arg	Phe				
		595					600					605							
Asp	Ser	Asp	Gly	Val	Leu	Leu	Gly	Ala	Phe	Ser	Asn	Gly	Arg	Thr	Leu				
	610					615					620								
Ala	Leu	Ala	Gln	Val	Ala	Leu	Ala	Asn	Phe	Ala	Asn	Asp	Ala	Gly	Leu				
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Gln	Ala	Leu	Gly	Gly	Asn	Val	Phe	Ser	Gln	Thr	Gly	Asn	Ser	Gly	Gln				
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Ala	Leu	Ile	Gly	Ala	Ala	Asn	Thr	Gly	Arg	Arg	Gly	Ser	Ile	Ser	Gly				
			660				665						670						
Ser	Lys	Leu	Glu	Ser	Ser	Asn	Val	Asp	Leu	Ser	Arg	Ser	Leu	Thr	Asn				

	675		680		685	
Leu	Ile	Val	Val	Gln	Arg	Gly
690						695
				Phe	Gln	Ala
				Asn	Ser	Lys
						700
Thr	Ser	Asp	Gln	Ile	Leu	Asn
705				710		715
					Leu	Lys
					Gln	*

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TATACCATGG TGCTTAGGTC TTTAT

25

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGAATTCAA TTGCTTAAGA TTCAA

25

CLAIMS

1. A *Helicobacter pylori* FlgE polypeptide, or a modified form thereof retaining functionally equivalent antigenicity, for use in inducing a protective immune response to *Helicobacter pylori* infection.
5
2. A *Helicobacter pylori* FlgE polypeptide according to claim 1 which has substantially the amino acid sequence shown in SEQ ID NO: 2 in the Sequence Listing, for use in inducing a protective immune response to *Helicobacter pylori* infection.
10
3. A vaccine composition for inducing a protective immune response to *Helicobacter pylori* infection, comprising an immunogenically effective amount of a *Helicobacter pylori* FlgE polypeptide as defined in claim 1 or 2, optionally together with a pharmaceutically acceptable carrier or diluent.
15
4. A vaccine composition according to claim 3 in addition comprising an adjuvant.
- 20 5. A vaccine composition according to claim 4 wherein the adjuvant is a pharmaceutically acceptable form of cholera toxin.
6. A vaccine composition according to any one of claims 3 to 5 for use as a therapeutic vaccine in a mammal, including man, which is infected by
25 *Helicobacter pylori*.

7. A vaccine composition according to any one of claims 3 to 5 for use as a prophylactic vaccine to protect a mammal, including man, from infection by *Helicobacter pylori*.
- 5 8. Use of a *Helicobacter pylori* FlgE polypeptide as defined in claim 1 or 2 in the manufacture of a composition for the treatment, prophylaxis or diagnosis of *Helicobacter pylori* infection.
9. Use of a *Helicobacter pylori* FlgE polypeptide as defined in claim 1 or 2 in the
10 manufacture of a vaccine for use in eliciting a protective immune response against *Helicobacter pylori*.
10. Use of a *Helicobacter pylori* FlgE polypeptide as defined in claim 1 or 2 in the
15 manufacture of a diagnostic kit for diagnosis of *Helicobacter pylori* infection.
11. A method of *in vitro* diagnosis of *Helicobacter pylori* infection comprising at least one step wherein a *Helicobacter pylori* FlgE polypeptide as defined in claim 1 or 2, optionally labelled or coupled to a solid support, is used.
- 20 12. A method according to claim 11 comprising the steps
 - (a) contacting a said *Helicobacter pylori* FlgE polypeptide, optionally bound to a solid support, with a body fluid taken from a mammal; and
 - (b) detecting antibodies from the said body fluid binding to the said FlgE polypeptide.
- 25 13. A diagnostic kit for the detection of *Helicobacter pylori* infection in a mammal, including man, comprising components which enable the method according to claim 11 or 12 to be carried out.

14. A diagnostic kit according to claim 13, comprising:

- (a) a *Helicobacter pylori* FlgE polypeptide; and
- (b) reagents for detecting antibodies binding to the said FlgE polypeptide.

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15. A method of eliciting in a mammal a protective immune response against *Helicobacter pylori* infection, said method comprising the step of administering to the said mammal an immunologically effective amount of a *Helicobacter pylori* FlgE polypeptide as defined in claim 1 or 2.

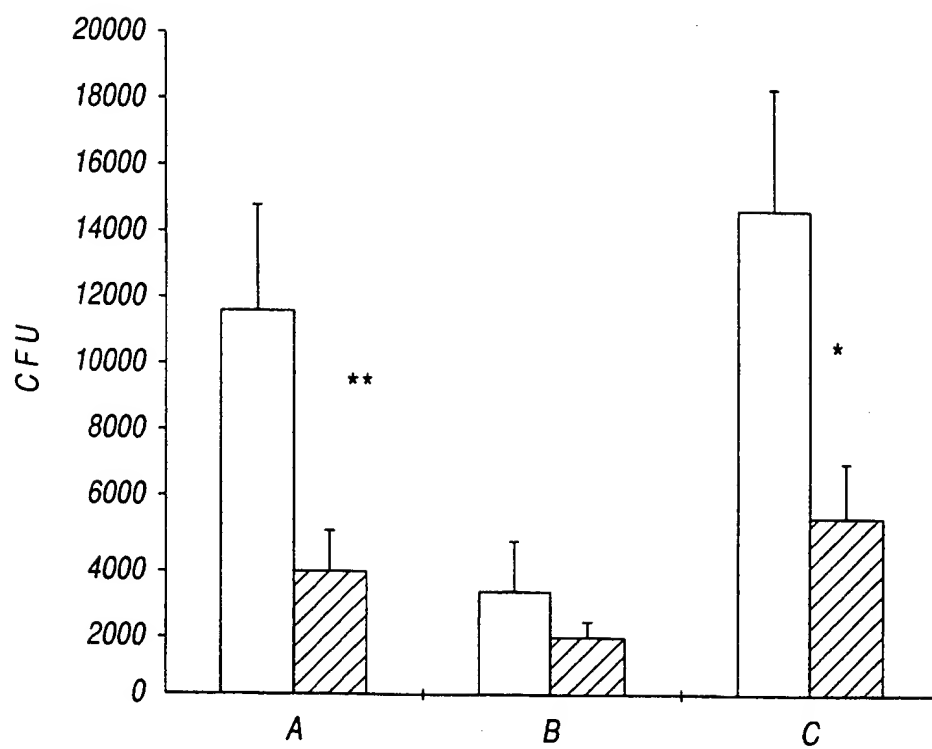
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16. A method of eliciting in a mammal a protective immune response against *Helicobacter pylori* infection, said method comprising the step of administering to the said mammal an immunologically effective amount of a vaccine composition according to any one of claims 3 to 7.

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17. A method according to claim 15 or 16 wherein the said mammal is a human.

1/2

*Fig.1*

2/2

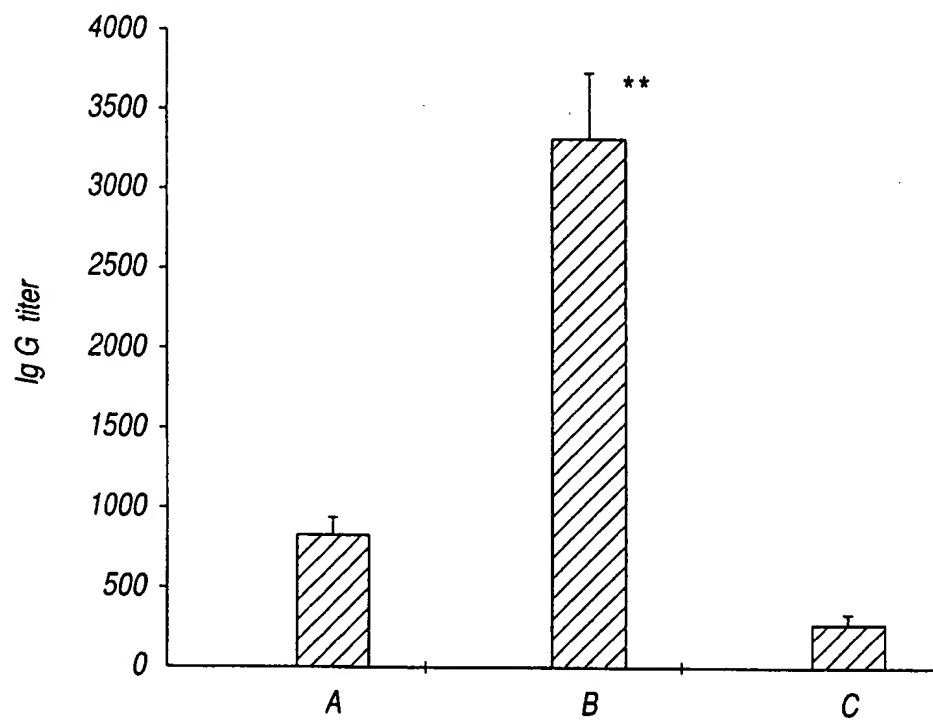


Fig.2